RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/507, 42/
Source: 10/507, 42/
Date Processed by STIC: 3-28-05

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 03/28/2005
PATENT APPLICATION: US/10/507,421 TIME: 14:23:50

Input Set : A:\2005-03-09 0760-0337PUS1.ST25.txt

Output Set: N:\CRF4\03282005\J507421.raw

```
4 <110> APPLICANT: NARIMATSU, Hisashi et al.
      6 <120> TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINE TRANSFERASE, NUCLEIC ACID ENCODING
THE
              SAME AND USE THEREOF IN DIAGNOSING CANCER AND/OR TUMOR
      9 <130> FILE REFERENCE: 0760-0337PUS1
     11 <140> CURRENT APPLICATION NUMBER: US 10/507,421
     12 <141> CURRENT FILING DATE: 2004-09-13
     14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/03044
     15 <151> PRIOR FILING DATE: 2003-03-14
     17 <150> PRIOR APPLICATION NUMBER: JP 2002-70996
     18 <151> PRIOR FILING DATE: 2002-03-14
     20 <160> NUMBER OF SEQ ID NOS: 28
     22 <170> SOFTWARE: PatentIn 3.2
     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 283
     26 <212> TYPE: PRT
     27 <213> ORGANISM: Homo sapiens
     29 <400> SEQUENCE: 1
     30 Tyr Phe Pro Met Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val
                          5
                                             10
     32 Tyr Leu Leu Val Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg
                     20
                                         25
     34 Glu Ala Ile Arg Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly
                                    40
     36 Gly Arg Gly Ala Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys
             50
                                 55
     38 Gln Glu Glu Arg Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg
                             70
                                                 75
     40 Leu Tyr Gly Asp Ile Leu Gln Trp Gly Phe Leu Asp Thr Phe Phe Asn
                                             90
     42 Leu Thr Leu Lys Glu Ile His Phe Leu Lys Trp Leu Asp Ile Tyr Cys
    43
                     100
                                        105
                                                             110
     44 Pro His Val Pro Phe Ile Phe Lys Gly Asp Asp Val Phe Val Asn
    45
               115
                                    120
     46 Pro Thr Asn Leu Leu Glu Phe Leu Ala Asp Arg Gln Pro Gln Glu Asn
            130
                                135
                                                    140
     48 Leu Phe Val Gly Asp Val Leu Gln His Ala Arg Pro Ile Arg Arg Lys
                            150
    50 Asp Asn Lys Tyr Tyr Ile Pro Gly Ala Leu Tyr Gly Lys Ala Ser Tyr
                        165
                                            170
    52 Pro Pro Tyr Ala Gly Gly Gly Phe Leu Met Ala Gly Ser Leu Ala
                    180
                                        185
                                                             190
```

54 Arg Arg Leu His His Ala Cys Asp Thr Leu Glu Leu Tyr Pro Ile Asp

200

195

Input Set : A:\2005-03-09 0760-0337PUS1.ST25.txt
Output Set: N:\CRF4\03282005\J507421.raw

					_												
56 57	Asp	Val 210	Phe	Leu	Gly	Met	Cys 215	Leu	Glu	Val	Leu	Gly 220	Val	Gln	Pro	Thr	
	Δla		Glu	Gly	Phe	Lvs		Phe	Glv	Tle	Ser		Asn	Ara	Asn	Ser	
	225		01.4	CTY	1110	230		1110	O± y		235	9	11011	9		240	
		Mot	7 0 0	T	C1		C	Dho	Dho	71 ~~ ~~		Mot	T 011	17 - 1	Wa l		
	Arg	Met	ASII	Lys		Pro	Cys	Pne	Pne	-	Ата	мес	Leu	vaı		uis	
61				_	245		_	_		250			_		255	_	
	Lys	Leu	Leu	Pro	Pro	Glu	Leu	Leu		Met	Trp	Gly	Leu		His	Ser	
63				260					265					270			
64	Asn	Leu	Thr	Cys	Ser	Arg	Lys	Leu	Gln	Val	Leu						
65			275					280									
67	<210)> SI	EQ II	ON C	2												
68	<213	l> LE	ENGTI	H: 84	19												
69	<212	2> T	YPE:	DNA													
				ISM:	Homo	o sar	oiens	3									
				NCE:													
				atg		cta	aac	cac	cca	nan	aad	tac	agg	aac	gat	atc	48
				Met													10
75	1	1110	110	1100	DCU.	шси	11011	1115	110	10	цуз	Cys	1119	O _T y	15	1 44	
	-	a+ a	a+ a	gtg	++~	a+ a	224	+ ~~	~+ ^		200	~~~	C2.C	a 2 a		000	96
																	30
	ıyı	ьeu	ьeu	Val	vaı	vaı	гуу	ser		тте	TIIL	GIII	птъ	_	Arg	ALG	
78				20					25					30			1.44
		-		cgc					-			_		_			144
	GLu	Ala		Arg	GIn	Thr	Trp	-	Arg	GLu	Arg	GIn		Ala	GTA	GTA	
81			35					40					45				
				gcc													192
83	Gly	Arg	Gly	Ala	Val	Arg	Thr	Leu	Phe	Leu	Leu	Gly	Thr	Ala	Ser	Lys	
84		50					55					60					
85	cag	gag	gag	cgc	acg	cac	tac	cag	cag	ctg	ctg	gcc	tac	gaa	gac	cgc	240
86	Gln	Glu	Glu	Arg	Thr	His	Tyr	Gln	Gln	Leu	Leu	Ala	Tyr	Glu	Asp	Arg	
87	65					70					75					80	
88	ctc	tac	ggc	gac	atc	ctg	cag	tgg	ggc	ttt	ctc	gac	acc	ttc	ttc	aac	288
89	Leu	Tyr	Gly	Asp	Ile	Leu	Gln	Trp	Gly	Phe	Leu	Asp	Thr	Phe	Phe	Asn	
90		_	_	_	85			_	_	90		_			95		
91	cta	acc	ctc	aag	gag	atc	cac	ttc	ctc	aaσ	taa	cta	gac	atc	tac	tac	336
				Lys													
93				100					105	-1-			1-	110	- 1	4	
	ccc	cac	atc	CCC	ttc	att	ttc	aaa		gac	σat	gac	atc		atc	aac	384
				Pro													
96		*****	115	110				120	_	1101	ПОР	1101	125	1	,	11011	
		200		ctg	cta	ma a				asc.	caa	cad		cad	~ a a	220	432
				Leu													452
99	FIO	130	MSII	пеп	ьеu	GIU	135	neu	міа	nsp	MIG	140	FIQ	GIII	GIU	ASII	
	٠				. ~~+	- ~+.				. ~~+	- ~~		+	- ~~		~ ~~~	480
																g aaa	400
			e va.	r GTZ	AS			ı GII	1 112	S Ala		-) ITE	e Arc	J AL	J Lys	
	2 145					150					15			•		160	500
																c tat	528
	-) Asr	ı Lys	з Туг	_		Pro	O GI	y Ala			c Gly	у Гуз	s Ala		r Tyr	
105					165					170					175		
106	cci	d cc	g tat	gca	a ggo	ggc	ggt	gg	tto	cto	c ato	g gco	ggg	ago	ct	g gcc	576

Input Set : A:\2005-03-09 0760-0337PUS1.ST25.txt
Output Set: N:\CRF4\03282005\J507421.raw

107 Pro Pro Tyr Ala Gly Gly Gly Phe Leu Met Ala Gly Ser Leu Ala 185 109 cgg cgc ctg cac cat gcc tgc gac acc ctg gag ctc tac ccg atc gac 624 110 Arg Arg Leu His His Ala Cys Asp Thr Leu Glu Leu Tyr Pro Ile Asp 200 112 gac gtc ttt ctg ggc atg tgc ctg gag gtg ctg ggc gtg cag ccc acg 672 113 Asp Val Phe Leu Gly Met Cys Leu Glu Val Leu Gly Val Gln Pro Thr 210 115 gcc cac gag ggc ttc aag act ttc ggc atc tcc cgg aac cgc aac agc 720 116 Ala His Glu Gly Phe Lys Thr Phe Gly Ile Ser Arg Asn Arg Asn Ser 230 235 118 cgc atg aac aag gag ccg tgc ttt ttc cgc gcc atg ctc gtg gtg cac 768 119 Arg Met Asn Lys Glu Pro Cys Phe Phe Arg Ala Met Leu Val Val His 245 250 121 aag ctg ctg ccc cct gag ctg ctc gcc atg tgg ggg ctg gtg cac agc 816 122 Lys Leu Leu Pro Pro Glu Leu Leu Ala Met Trp Gly Leu Val His Ser 260 265 124 aat ctc acc tgc tcc cgc aag ctc cag gtg ctc 849 125 Asn Leu Thr Cys Ser Arg Lys Leu Gln Val Leu 275 280 128 <210> SEQ ID NO: 3 129 <211> LENGTH: 327 130 <212> TYPE: PRT 131 <213> ORGANISM: Homo sapiens 133 <400> SEQUENCE: 3 134 Ala Ser Gln Gly Pro Gln Ala Trp Asp Val Thr Thr Asn Cys Ser 10 136 Ala Asn Ile Asn Leu Thr His Gln Pro Trp Phe Gln Val Leu Glu Pro 20 138 Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro Met 35 40 140 Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu Val 55 142 Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile Arg 75 70 144 Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala 146 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 147 100 105 148 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 120 150 Ile Leu Gln Trp Gly Phe Leu Asp Thr Phe Phe Asn Leu Thr Leu Lys 135 152 Glu Ile His Phe Leu Lys Trp Leu Asp Ile Tyr Cys Pro His Val Pro 150 153 145 155 154 Phe Ile Phe Lys Gly Asp Asp Val Phe Val Asn Pro Thr Asn Leu 170 156 Leu Glu Phe Leu Ala Asp Arg Gln Pro Gln Glu Asn Leu Phe Val Gly 157 180 185

Input Set : A:\2005-03-09 0760-0337PUS1.ST25.txt

Output Set: N:\CRF4\03282005\J507421.raw

158 Asp Val Leu Gln His Ala Arg Pro Ile Arg Arg Lys Asp Asp Lys Tyr 199 195 200 205 200 205 200 205 200 205 200 205 200 205 240 215 220 230 235 240 240 240 245 250 245 250 255 240 266 245 266 245 250 255 266 Gly Asp Asp Thr Leu Glu Leu Tyr Pro Thr Ala His Glu Gly 245 250 255 266 Gly Asp Thr Leu Glu Leu Tyr Pro Thr Ala His Glu Gly 265 270 266 275 260 265 270 266 275 260 265 270 266 275 260 265 270 266 275 260 265 270 266 275 260 285 270 266 275 260 285 270 266 275 260 285 270 266 275 280 285 270																		
161 210 215 220 162 Gly Gly Gly Gly Phe Leu Met Ala Gly Ser Leu Ala Arg Arg Leu His 230 235 230 240 164 His Ala Cys Asp Thr Leu Glu Leu Tyr Pro Tle Asp Asp Val Phe Leu 165 245 250 255 166 Gly Met Cys Leu Glu Val Leu Gly Val Gln Pro Thr Ala His Glu Gly 267 260 265 280 280 168 Phe Lys Thr Phe Gly Ile Ser Arg Asn Arg Asn Ser Arg Met Asn Lys 280 275 280 285 170 Glu Pro Cys Phe Phe Arg Ala Met Leu Val Val His Lys Leu Leu Pro 171 290 295 300 172 Pro Glu Leu Leu Ala Met Trp Gly Leu Val His Ser Asn Leu Thr Cys 310 300 173 Ser Arg Lys Leu Gln Val Leu 175 325 320 174 Ser Arg Lys Leu Gln Val Leu 175 325 320 175 Yer Cys Phe Phe Arg Ala Met Trp Gly Leu Val His Ser Asn Leu Thr Cys 310 320 174 Ser Arg Lys Leu Gln Val Leu 175 325 320 175 Seo ID NO: 4 178 <211> LENGTH: 981 180 <212> TYPE: DNA 180 <213> ORGANISM: Homo sapiens 182 <400> SEQUENCE: 4 184 Ala Ser Gln Gly Pro Gln Ala Trp Asp Val Thr Thr Asn Cys Ser 185 1 5 1 5 1 5 1 6 1 5 5 1 7 5 1 8 6 gcc aat atc aac ttg acc cac cag ccc tgg ttc cag gtc ctg aga ccg 96 187 Ala Asn Ile Asn Leu Thr His Gln Pro Trp Phe Gln Val Leu Glu Pro 25 189 cag ttc cgg cag ttt ctc ttc tac cgc cac tgc cgc tac ttc ccc atg 144 190 Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro Met 191 35 40 45 192 ctg ctg aac cac cac gag aag tgc agg gag gtg gad gtc atc ctc ctg tgg gad gag gad gad gad gad gad gad gad g		Asp	Val		Gln	His	Ala	Arg		Ile	Arg	Arg	Lys		Asn	Lys	Tyr	
163 225 230 235 240 245	160	Tyr		Pro	Gly	Ala	Leu		Gly	Lys	Ala	Ser		Pro	Pro	Tyr	Ala	
165		_	Gly	Gly	Gly	Phe		Met	Ala	Gly	Ser		Ala	Arg	Arg	Leu		
167		His	Ala	Cys	Asp		Leu	Glu	Leu	Tyr		Ile	Asp	Asp	Val		Leu	
169		Gly	Met	Cys		Glu	Val	Leu	Gly		Gln	Pro	Thr	Ala		Glu	Gly	
171		Phe	Lys		Phe	Gly	Ile	Ser		Asn	Arg	Asn	Ser		Met	Asn	Lys	
173 305 310 Val Leu 174 Ser Arg Lys Leu Gln Val Leu 175 325 177 <210> SEQ ID NO: 4 178 <2211> LENGTH: 981 179 <212> TYPE: DNA 180 <213> ORGANISM: Homo sapiens 182 <400> SEQUENCE: 4 183 gcc tct cag ggg ccc cag gcc tgg gac gtg acc acc act aac tgc tca 184 Ala Ser Gln Gly Pro Gln Ala Trp Asp Val Thr Thr Thr Asn Cys Ser 185 1 5 10 15 186 gcc aat atc aac ttg acc cac cag ccc tgg ttc cag gtc ctg gag ccg 187 Ala Asn Ile Asn Leu Thr His Gln Pro Trp Phe Gln Val Leu Glu Pro 188 20 25 189 cag ttc cgg cag ttt ctc ttc tac cgc cac tgc cgc tac ttc ccc atg 190 Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro Met 191 35 192 ctg ctg aac cac ccc gag aag tgc aag ggc gat gtc tac ctc ctg ctg gtg 194 50 55 195 gtt gtc aag tcg gtc atc acc cag cac gac cac gac cgc gag gcc atc ctc ctc 195 gtt gtc aag tcg gtc atc acc acc cag cac gac cgc cgc gag gcc atc cgc 196 Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile Arg 197 65 70 70 75 80 198 cag acc tgg ggc cgc gag cgc gat gcc tca acc acc cac cac cac cac cac cac c		Glu		Суѕ	Phe	Phe	Arg		Met	Leu	Val	Val		Lys	Leu	Leu	Pro	
175			Glu	Leu	Leu	Ala		Trp	Gly	Leu	Val		Ser	Asn	Leu	Thr	_	
178 <211> LENGTH: 981 179 <212> TYPE: DNA 180 <213> ORGANISM: Homo sapiens 182 <400> SEQUENCE: 4 183 gcc tct cag ggg ccc cag gcc tgg gac gtg acc acc act aac tgc tca 184 Ala Ser Gln Gly Pro Gln Ala Trp Asp Val Thr Thr Thr Asn Cys Ser 185 1		Ser	Arg	Lys	Leu		Val	Leu										
179	177	<210)> SE	EQ II	ON C	: 4												
180 <213> ORGANISM: Homo sapiens 182 <400> SEQUENCE: 4 183 gcc tct cag ggg ccc cag gcc tgg gac gtg acc acc act aac tgc tca 184 Ala Ser Gln Gly Pro Gln Ala Trp Asp Val Thr Thr Thr Asn Cys Ser 185 1	178																	
182	179																	
182	180	<213	3> OF	RGAN	ISM:	Homo sapiens												
183 gcc tct cag ggg ccc cag ggc tgg gac gtg acc acc acc acc acc acc acc acc acc ac						-												
184 Ala Ser Gln Gly Pro Gln Ala Trp Asp Val Thr Thr Thr Asn Cys Ser 185 1 5 10 15 15 166 gcc aat atc aac ttg acc cac cag ccc tgg ttc cag gtc ctg gag ccg 96 187 Ala Asn Ile Asn Leu Thr His Gln Pro Trp Phe Gln Val Leu Glu Pro 188 20 30 144 189 Cag ttc cgg cag ttt ctc ttc ttc tac cgc cac tgc cgc tac ttc ccc atg 144 190 Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro Met 191 35 40 45 192 ctg ctg aac cac ccg gag aag tgc agg ggc gat gtc tac ctg ctg gtg 192 193 Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu Val 194 50 55 60 195 gtt gtc aag tcg gtc atc acc cag cag cag cag cag cag cag cag gag g							caq	acc	t.aa	gac	ata	acc	acc	act	aac	tac	t.ca	48
185 1																		
187 Ala Asn Ile Asn Leu Thr His Gln Pro Trp Phe Gln Val Leu Glu Pro 188	185	1			_	5			_	_	10					15		0.6
188 20 25 30 189 cag ttc cgg cag ttt ctc ttc ttc tac cgc cac tgc cgc tac ttc ccc atg 144 190 Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro Met 191 191 35 40 45 192 ctg ctg aac cac cac ccg gag aag tgc agg ggc gat gtc tac ctg ctg gtg 192 193 Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu Val 194 194 50 55 60 195 gtt gtc aag tcg gtc atc acg cag cac cac gac cgc cgc gag gcc atc cgc 240 196 Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile Arg 70 75 80 198 cag acc tgg ggc cgc gag cgg cgg cag tcc ggg ggg ggc cga ggc gcc 288 199 Gln Thr Trp Gly Arg Glu Arg Gln Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala 85 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag cgc 336 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 336 203																		96
190 Gln Phe Arg Gln Phe Leu Phe Tyr Arg His Cys Arg Tyr Phe Pro Met 191	188				20					25	_				30			
191	189	cag	ttc	cgg	cag	ttt	ctc	ttc	tac	cgc	cac	tgc	cgc	tac	ttc	CCC	atg	144
192 ctg ctg aac cac ccg gag aag tgc agg ggc gat gtc tac ctg ctg gtg 193 Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu Val 194		Gln	Phe	-	Gln	Phe	Leu	Phe	_	Arg	His	Cys	Arg	_	Phe	Pro	Met	
193 Leu Leu Asn His Pro Glu Lys Cys Arg Gly Asp Val Tyr Leu Leu Val 194 50 55 60 195 gtt gtc aag tcg gtc atc acg cag cac gac cgc cgc gag gcc atc cgc 196 Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile Arg 197 65 70 75 80 198 cag acc tgg ggc cgc gag cgg cag tcc gcg ggt ggg ggc cga ggc gcc 199 Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala 200 85 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag ggc cgc 336 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 384 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc tc aag cag 432		cta	cta		cac	cca	aaa	aan		ann	aac	cat	atc		cta	cta	ata	192
194 50 55 60 195 gtt gtc aag tcg gtc atc acg cac gac cgc cgc gag gcc atc cgc 240 196 Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile Arg 240 197 65 70 75 80 198 cag acc tgg ggc cgc gag cgg cag tcc gcg ggt ggg ggc cga ggc gcc 288 199 Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag cgc 336 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 384 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 384 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc ttc aac ctg acc ctc aag 432																		172
196 Val Val Lys Ser Val Ile Thr Gln His Asp Arg Arg Glu Ala Ile Arg 197 65 70 75 80 198 cag acc tgg ggc cgc gag cgg cag tcc gcg ggt ggg ggc cga ggc gcc 288 199 Gln Thr Trp Gly Arg Glu Arg Glu Ser Ala Gly Gly Gly Arg Gly Ala 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag cgc 336 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 336 203	194		50					55	_	_	_	_	60	_				
197 65 70 75 80 198 cag acc tgg ggc cgc gag cgg cag tcc gcg ggt ggg ggc cga ggc gcc 288 199 Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala 200 85 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag cgc 336 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 110 203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 384 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 384 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aag ctg acc ctc aag 432																		240
198 cag acc tgg ggc cgc gag cgg cag tcc gcg ggt ggg ggc cga ggc gcc 288 199 Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala 200 85 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag ggc cgc 336 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 384 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	196	Val	Val	Lys	Ser	Val	Ile	Thr	Gln	His	Asp	Arg	Arg	Glu	Ala	Ile	Arg	
199 Gln Thr Trp Gly Arg Glu Arg Gln Ser Ala Gly Gly Gly Arg Gly Ala 200 85 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag cgc 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	197	65					70					75					80	
200 85 90 95 201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag cgc 336 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 384 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432																		288
201 gtg cgc acc ctc ttc ctg ctg ggc acg gcc tcc aag cag gag gag cgc 202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	199	Gln	Thr	Trp	Gly	Arg	Glu	Arg	Gln	Ser	Ala	Gly	Gly	Gly	Arg	Gly	Ala	
202 Val Arg Thr Leu Phe Leu Leu Gly Thr Ala Ser Lys Gln Glu Glu Arg 203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	200					85		•			90					95		
203 100 105 110 204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 384 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	201	gtg	cgc	acc	ctc	ttc	ctg	ctg	ggc	acg	gcc	tcc	aag	cag	gag	gag	cgc	336
204 acg cac tac cag cag ctg ctg gcc tac gaa gac cgc ctc tac ggc gac 384 205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	202	Val	Arg	Thr	Leu	Phe	Leu	Leu	Gly	Thr	Ala	Ser	Lys	Gln	Glu	Glu	Arg	
205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	203				100					105					110			
205 Thr His Tyr Gln Gln Leu Leu Ala Tyr Glu Asp Arg Leu Tyr Gly Asp 206 115 120 125 207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432	204	acg	cac	tac	cag	cag	ctg	ctg	gcc	tac	gaa	gac	cgc	ctc	tac	ggc	gac	384
207 atc ctg cag tgg ggc ttt ctc gac acc ttc ttc aac ctg acc ctc aag 432																		
	206			115					120			-	-	125				
	207	atc	ctg	cag	tgg	ggc	ttt	ctc		acc	ttc	ttc	aac	ctg	acc	ctc	aag	432

Input Set : A:\2005-03-09 0760-0337PUS1.ST25.txt

Output Set: N:\CRF4\03282005\J507421.raw

000 100																	
209		130					135					140					
								ctg									480
		Ile	His	Phe	Leu	-	Trp	Leu	Asp	Ile	_	Cys	Pro	His	Val		
	145					150					155					160	
213	ttc	att	ttc	aaa	ggc	gac	gat	gac	gtc	ttc	gtc	aac	CCC	acc	aac	ctg	528
214	Phe	Ile	Phe	Lys	Gly	Asp	Asp	Asp	Val	Phe	Val	Asn	Pro	Thr	Asn	Leu	
215	•				165					170				•	175		
216	cta	gaa	ttt	ctg	gct	gac	cgg	cag	cca	cag	gaa	aac	ctg	ttc	gtg	ggc	576
								Gln									
218				180		-	_		185					190		_	
219	gat	qtc	ctq	caq	cac	qct	cqq	ccc	att	cqc	agg	aaa	qac	aac	aaa	tac	624
								Pro									
221	•		195				•	200		_		-	205		-	-	
222	tac	atc	cca	aaa	acc	cta	tac	ggc	aaσ	acc	aσc	tat	cca	cca	tat	σca	672
			_		_	_		Gly	_	_	_		_	_		_	
224	-1-	210		1			215	1	-1-			220			- 1 -		
	aac		aat	aac	ttc	ctc	atσ	gcc	aac	aσc	cta	acc	caa	cac	cta	cac	720
								Ala									
	225	1	4 -1	4 -1		230			4-1	002	235		9	9	200	240	
		acc	tac	gac	acc		σασ	ctc	tac	aca		gac	gac	atc	+++		768
								Leu									
230			0,0	1105	245		014	200	-1-	250		1100	110P	• • • •	255	Lou	
	aac	ato	tac	cta		ata	cta	ggc	ata		CCC	acq	acc	cac		aac	816
								Gly									010
233	011	1100	0,0	260	014			0-1	265	02		****	*****	270	02.4		
	ttc	aad	act		aac	atc	tcc	cgg		cac	aac	agc	cac		aac	aan	864
								Arg									001
236	1110	цуо	275	1110	O ± y	110	001	280	71011	1119	11011	561	285	1100	11011	шуз	
	nan	cca		+++	ttc	cac	acc	atg	ctc	ata	ata	Cac		cta	cta	CCC	912
								Met									712
239	OIU	290	Cys	1110	LIIC	nry	295	HCC	ыси	Val	Val	300	цуз	цец	цеа	110	
	cct		cta	ctc	000	ata		ggg	cta	a+a	020		22+	ata	300	tac	960
								Gly									900
	305	GIU	пеп	пеи	ΑΙα	310	тър	Сту	пеп	val	315	Ser	NSII	пеа	TIIL	320	
	tcc	000	224	ata	020		a+ a				213					320	981
	Ser											•					901
245	ser	Arg	пуз	пеп	325	vai	пеп										
	<210)	70 TI) NO													
	<211																
					200												
	<212				Uome		.i.	_							•		
	<400					Sal	piens	o'									
													.				4.0
								gtc									48
		ser	ьeu	Trp		гуѕ	Thr	Val	Tyr	_	Ser	ьеи	Cys	ьeu		Leu	
255	1	_4-	_4-	d	5	- 4		1 .		10		4.			15	+	0.0
								gtg									96
	Ата	ьeu	ьeu		Ата	vaı	Tnr	Val		GIN	Arg	ser	ьeu		Pro	GTA	
258				20					25					30			
∠59	cag	ttt	ctg	cag	gag	cct	ccg	cca	ccc	acc	ctg	gag	cca	cag	aag	gcc	144

VERIFICATION SUMMARY

DATE: 03/28/2005

PATENT APPLICATION: US/10/507,421

TIME: 14:23:51

Input Set : A:\2005-03-09 0760-0337PUS1.ST25.txt

Output Set: N:\CRF4\03282005\J507421.raw